

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 18, 2001, 15:57:52 ; Search time 31.07 seconds
(without alignments)
3253.332 Million cell updates/sec

Title: US-09-587-111-5

Perfect score: 4004
Sequence: 1 MTSPPSSPVFRLETLTGCGE.....EDEDGASEENVVPVQLQSN 764

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 133305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_16:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.todent:*
13: sp.unclassified:*
14: sp.vertebrate:*
15: sp.virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4004	100.0	764	4 Q9Y5S1	Q9Y5S1 homo sapien
2	3945	98.5	764	4 Q9Y670	Q9Y670 homo sapien
3	3159	78.9	756	11 Q9WTR1	Q9WTR1 mus musculu
4	3051.5	76.2	761	11 Q9WUD2	Q9WUD2 mus musculu
5	3041.5	76.0	761	11 Q9QYH8	Q9QYH8 rattus norv
6	3028.5	75.6	762	11 Q9JMT8	Q9JMT8 rattus norv
7	1652	41.3	838	11 Q35433	Q35433 rattus norv
8	1652	41.3	838	11 Q9JMS7	Q9JMS7 rattus norv
9	1651.5	41.2	839	4 Q9H304	Q9H304 homo sapien
10	1648.5	41.2	839	4 Q9H0G9	Q9H0G9 homo sapien
11	1644.5	41.1	839	4 Q9H074	Q9H074 homo sapien
12	1636.5	40.9	839	4 Q9NY22	Q9NY22 homo sapien
13	1467	36.6	852	13 Q9DFS3	Q9DFS3 gallus gall
14	1467	36.6	871	4 Q9HBC0	Q9HBC0 homo sapien
15	1465.5	36.6	871	11 Q9ERZ8	Q9ERZ8 rattus norv
16	1464	36.6	871	4 Q9HBA0	Q9HBA0 homo sapien
17	1458.5	36.4	871	11 Q9ES76	Q9ES76 mus musculu
18	1457.5	36.4	871	11 Q9EPK8	Q9EPK8 mus musculu
19	1452.5	36.3	871	11 Q9EQZ4	Q9EQZ4 mus musculu

20-	1446.5	36.1	873	11 Q9ERZ7	Q9ERZ7 mus musculu
21	1442.5	36.0	778	11 Q9JMS6	Q9JMS6 rattus norv
22	1112.5	27.8	528	11 Q9Z1B2	Q9Z1B2 rattus norv
23	969	24.2	511	4 Q9H303	Q9H303 homo sapien
24	933	23.3	471	11 Q9JLM0	Q9JLM0 rattus norv
25	634	15.8	725	4 Q9H296	Q9H296 homo sapien
26	631	15.8	725	4 Q9H1D1	Q9H1D1 homo sapien
27	630	15.7	725	4 Q9H1D0	Q9H1D0 homo sapien
28	607.5	15.2	727	11 Q9R1B6	Q9R1B6 rattus norv
29	589	14.7	723	11 Q9J1P0	Q9J1P0 rattus norv
30	586	14.6	730	6 Q9XSM3	Q9XSM3 oryctolagus
31	584	14.6	723	11 Q9J1L2	Q9J1L2 rattus norv
32	579.5	14.5	729	4 Q9NOA5	Q9NOA5 homo sapien
33	469.5	11.7	769	5 Q9N3Y9	Q9N3Y9 caenorhabd
34	440.5	11.0	729	11 Q9J1J0	Q9J1J0 mus musculu
35	428.5	10.7	750	5 Q9VUD5	Q9VUD5 drosophila
36	414	10.3	900	5 Q61220	Q61220 caenorhabd
37	392.5	9.8	790	5 P90784	P90784 caenorhabd
38	364	9.1	937	5 Q17469	Q17469 caenorhabd
39	338	8.4	1123	5 Q9W3W0	Q9W3W0 drosophila
40	261	6.5	519	5 Q22374	Q22374 caenorhabd
41	255	6.4	1913	5 Q9GRV5	Q9GRV5 caenorhabd
42	233	5.8	904	5 Q9W0T5	Q9W0T5 drosophila
43	229	5.7	1453	5 Q9VMR4	Q9VMR4 drosophila
44	226.5	5.7	981	6 P79100	P79100 bos taurus
45	224.5	5.6	890	11 Q9QUQ9	Q9QUQ9 mus musculu

ALIGNMENTS

RESULT 1
Q9Y5S1 PRELIMINARY: PRT: 764 AA.

AC Q9Y5S1;
ID Q9Y5S1;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE VANILLOID RECEPTOR-LIKE PROTEIN 1.
GN VRL-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9215558; PubMed=10201375;
RA Caterina M.J., Rosen T.A., Tominaga M., Brake A.J., Julius D.;
RT "A capsaicin-receptor homologue with a high threshold for noxious heat.";
RT Nature. 398:436-441(1999).
RL EMBL: AF129112; AAD26363.1; -.
DR InterPro: IPR002110; -.
DR InterPro: IPR002111; -.
DR Pfam: PF00023; ank. 3.
DR PROSITE: PS50088; ANK_REPEAT. 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION. 1.
DR SMART: SM00248; ANK. 1.
KW Receptor.
SQ SEQUENCE 764 AA: 85980 MW; A73E3696E70F91E9 CRC64;

Query Match 100.0%; Score 4004; DB 4; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTSPPSSPVFRLETLTGCGEADRGKLDGSGLPMPESQFGEDRRKFAPIRVNLNY 60
|||||
DB 1 MTSPPSSPVFRLETLTGCGEADRGKLDGSGLPMPESQFGEDRRKFAPIRVNLNY 60
|||||
QY 61 RKTGASQDPNFRDRLFNNAVSRGVPEDLAGLPYLSKTSKYLLTDSYTBGSGTKTCL 120
|||||
DB 61 RKTGASQDPNFRDRLFNNAVSRGVPEDLAGLPYLSKTSKYLLTDSYTBGSGTKTCL 120
|||||

OY	121	MKVLYNLKDGYNACLPRLTLOIDRSGNQPLVMAQCDDYRGHSAHIAIEKRSLOCVK	180
OY	121	MKVLYNLKDGYNACLPRLTLOIDRSGNQPLVMAQCDDYRGHSAHIAIEKRSLOCVK	180
Db	121	MKAIVNLKDGYNACLPRLTLOIDRSGNQPLVMAQCDDYRGHSAHIAIEKRSLOCVK	180
OY	181	LLVENGAVVHARACGRFFQKQSGTCFEGYELPLSLACTKQMDVSVSLLENPHQPSLQA	240
Db	181	LLVENGAVVHARACGRFFQKQSGTCFEGYELPLSLACTKQMDVSVSLLENPHQPSLQA	240
OY	241	TDSQGNIVYLAHLMISDNSENIALVYSMDGLLQAGARLCPVQLEDIRNLQDLPRLKL	3000
Db	241	TDSQGNIVYLAHLMISDNSENIALVYSMDGLLQAGARLCPVQLEDIRNLQDLPRLKL	3000
OY	301	AAKEKEIEIPRHIILORESGSLHSRKTEWCYCPVRSYLDIASVSCSENSVLEETIAF	360
Db	301	AAKEKEIEIPRHIILORESGSLHSRKTEWCYCPVRSYLDIASVSCSENSVLEETIAF	360
OY	361	HCKSPHRRRMVLEPLNLLOAKMDLIPKFFLNLCLYMFETFFAVAHQPLTKQQA	420
Db	361	HCKSPHRRRMVLEPLNLLOAKMDLIPKFFLNLCLYMFETFFAVAHQPLTKQQA	420
OY	421	PHLKAQVNSMLTGHILLIGGIYLLVGLQWLYFMRHVFIIWISFIDSYFEILLFQALL	480
Db	421	PHLKAQVNSMLTGHILLIGGIYLLVGLQWLYFMRHVFIIWISFIDSYFEILLFQALL	480
OY	481	TIVSOVLCFLIAEWLPLVSAIVGMNLITYRGSOHNGIYSVMIOKYLRLPRL	540
Db	481	TIVSOVLCFLIAEWLPLVSAIVGMNLITYRGSOHNGIYSVMIOKYLRLPRL	540
OY	541	IYIVLFLFGFAVALVLSLOSEARPEAPGPNATSEVQPMEGODEGNAQYRGILIASLET	600
Db	541	IYIVLFLFGFAVALVLSLOSEARPEAPGPNATSEVQPMEGODEGNAQYRGILIASLET	600
OY	601	FKFTTGMGELAPFOBOJHFRGAVLLLLLAVLLYVILLNLMLIAMSETSVATDSMSIW	660
Db	601	FKFTTGMGELAPFOBOJHFRGAVLLLLLAVLLYVILLNLMLIAMSETSVATDSMSIW	660
OY	661	KLOKAIISYLEENGGWMCRRKQKQAGVMLTVGTRKDGSPDEDMWCRRVEEVMASMEQTLPT	720
Db	661	KLOKAIISYLEENGGWMCRRKQKQAGVMLTVGTRKDGSPDEDMWCRRVEEVMASMEQTLPT	720
OY	721	LCEDPSGAGVPRTEENPLVPLASPKPEDEDEGASEENYVPVQLQSN 764	
Db	721	LCEDPSGAGVPRTEENPLVPLASPKPEDEDEGASEENYVPVQLQSN 764	
RESULT	2		
O9Y670			
ID	O9Y670	PRELIMINARY:	PRT: 764 AA.
AC	O9Y670:		
DT	01-NOV-1999 (TReMBLrel. 12, Created)		
DT	01-NOV-1999 (TReMBLrel. 12, Last sequence update)		
DT	01-MAR-2001 (TReMBLrel. 16, Last annotation update)		
DE	VANILLOID RECEPTOR-LIKE PROTEIN.		
GN	VRL.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RA	Gloria R.L., Delmas P., Cesare P., Englund S., Liapi A., Wood J.N.;		
RT	*Cloning and functional expression of VRL, a vanilloid receptor-like		
RT	gene."		
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF103906; AAD41724.1; "		
DR	InterPro: IPR002110; "		
DR	InterPro: IPR002111; "		
DR	Pfam: PF00023; ank. 3.		
DR	PROSITE: PSS0088; ANK_REPEAT. 1.		
DR	PROSITE: PSS0297; ANK_REPEAT_REGION. 1.		
DR	SMART: SM00248; ANK. 1.		
FW	Receptor.		

SEQ	SEQUENCE	764 AA:	86053 MW:	AF9DBDF495EB43A0 CRC64:
Query Match		98.5%;	Score 3945;	DB 4; Length 764;
Best Local Similarity		98.2%;	Pred. No. 0;	
Matches 750; Conservative		6;	Mismatches 8;	Indels 0; Gaps 0
QY	1	MSPSSSPVFRLETTLDGGEDGSEADRGKLDIFGSGLPMPESQFQGRKFAFQIRVNLNY	60	
DB	1	MSPSSSPVFRLETTLDGGEDGSEADRGKLDIFGSGLPMPESQFQGRKFAFQIRVNLNY	60	
QY	61	RKGTGASQDDPRPRDRRLFNVASRGVPEDDLGLPEYLSKTSKYLTDSEYTGSGSTKCTL	120	
DB	61	RKGTGASQDDPRPRDRRLFNVASRGVPEDDLGLPEYLSKTSKYLTDSEYTGSGSTKCTL	120	
QY	121	MAVNLMLKGVNACLPLQLQIDRDSGNPQPLVNAOCTDDYRGHSAHLAIEKRSLOQVK	180	
DB	121	MAVNLMLKGVNACLPLQLQIDRDSGNPQPLVNAOCTDDYRGHSAHLAIEKRSLOQVK	180	
QY	181	LLVENGANYHARACGRFQGGTCFYFGEPLSLAACKQMDVVSYLENHPQASLOA	240	
DB	181	LLVENGANYHARACGRFQGGTCFYFGEPLSLAACKQMDVVSYLENHPQASLOA	240	
QY	241	TTSQGNTVLHALVMTSDNSAENIALVSMYDGLQAGALCPYQLEDIRNLQDLPLKL	300	
DB	241	TTSQGNTVLHALVMTSDNSAENIALVSMYDGLQAGALCPYQLEDIRNLQDLPLKL	300	
QY	301	AAKEGKIEIFRHILIDREFSGLSHLRSKPFEMQCYGPRVSLYLDASVDSCEENSLETIAF	360	
DB	301	AAKEGKIEIFRHILIDREFSGLSHLRSKPFEMQCYGPRVSLYLDASVDSCEENSLETIAF	360	
QY	361	HCKSPHRHRMVLEPLNKLQAKWMDLLPKFPLNFCNLIMEIFTAFAVYHQPTLKKQAA	420	
DB	361	HCKSPHRHRMVLEPLNKLQAKWMDLLPKFPLNFCNLIMEIFTAFAVYHQPTLKKQAA	420	
QY	421	PLKAEVGNMSMLTGHILLGLGTYLVGQMWYFMRHRYFMISFDSIFELLFLQALL	480	
DB	421	PLKAEVGNMSMLTGHILLGLGTYLVGQMWYFMRHRYFMISYDSEYELLFLHSL	480	
QY	481	TIVSVOLICLALIEWLPLILVSALVIGMLMLLYTTGFEQHTGYSVWIOKVIIRDLRFL	540	
DB	481	TIVSVOLICLALIEWLPLILVSALVIGMLMLLYTTGFEQHTGYSVWIOKVIIRDLRFL	540	
QY	541	ILVLFELFGFAVALVSLDSQEAPEAPPTGNATSESVQPMGQDEGNGAGYRGILSESL	600	
DB	541	ILVLFELFGFAVALVSLDSQEAPEAPPTGNATSESVQPMGQDEGNGAGYRGILSESL	600	
QY	601	EFTTGMGELAFQEODLHFRGNVLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW	660	
DB	601	EFTTGMGELAFQEODLHFRGNVLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW	660	
QY	661	KLQKRIASVLEMENGWMCCKKORACVMTLVGKPPGSGPERMCPRFEEVNMASWEOTLPT	720	
DB	661	KLQKRIASVLEMENGWMCCKKORACVMTLVGKPPGSGPERMCPRFEEVNMASWEOTLPT	720	
QY	721	LCEDPSGAGVPTLENPVLASPKKEDGASENTVPVQLOLSN	764	
DB	721	LCEDPSGAGVPTLENPVLASPKKEDGASENTVPVQLOLSN	764	
RESULT	3			
ID	Q9WTR1	PRELIMINARY;	PRT;	756 AA.
AC	Q9WTR1			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)		
DE	GROWTH FACTOR REGULATED CALCIUM CHANNEL.			
GN	VRLL OR GRC.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI	TaxID=10090;			

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57 BLACK-6; TISSUE=SPLEEN;
 RA Kanazaki M., Zhang Y., Kojima I.;
 RT "Growth factor regulated calcium channel.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021665; BAA78478.1; -
 DR MGI; MGI:1341836; Vrl.1.
 DR InterPro; IPR002110; -
 DR InterPro; IPR002111; -
 DR Pfam; PF00023; ank; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_REP_REGION; 1.
 DR SMART; SM00248; ANK; 1.
 SQ SEQUENCE 756 AA; 85964 MW; 4C037D0F6066EF4C CRC64;

Query Match 78.9%; Score 3159; DB 11; Length 756;
 Best Local Similarity 80.3%; Pred. No. 7.2e-241;
 Matches 615; Conservative 55; Mismatches 84; Indels 12; Gaps 5;

QY 1 MTSPPSPVFRLETTIDGGDEGSEADRGKLDGSGGLPMEHQFQEDRKFAQIRVNLNY 60
 DB 1 MTSASNPAPFRLETSDDGEGSAEVNKKG----NEPPMSEPFQEDRNFSPOIKVNLNY 56
 QY 61 RKGTGASQDPNRPDRDLFNVAVSRGVPEDLAQLPEYLSKTSKYLTDSYTGSGTGKTL 120
 DB 57 RKGLQPSQDDPNRPDRDLFSVYSRQVPEELTGLLEYLRTSKYLTDSYTGSGTGKTL 116
 QY 121 MKAVLNLDKDVNACILPLQLIDRDSGNPQPLVNAQCTDDYRQSHALIAIEKRSLOQV 180
 DB 117 MKAVLNLDQGVNACILPLQLIDRDSGNPQPLVNAQCTDEFYRQSHALIAIEKRSIMCVK 176
 QY 181 LLEVNGANVHAACGRFFQKGGTCTFEGELPLSLAACKTQMDVYVSYLLENHQAPSLQA 240
 DB 177 LLEVNGANVHAACGRFFQKHQGTCTFEGELPLSLAACKTQMDVYVSYLLENHQAPSLQA 236
 QY 241 TDSQGTVYHALVMTSDNSAENIALVTSMDGLQAGARLCTPVQEDIRNLQDILPLKL 300
 DB 237 TDSLQNTVYHALVMTADNSPENSALVIMYDLSLQMGARLCTPVQEDICNQGILPLKL 296
 QY 301 AAKEGKIEIFRHILOREFSG--SHLSRKFTWCYGPVAVSYLDLASVDSCEENSVLEIIA 359
 DB 297 AAKEGKIEIFRHILOREFSGLYOPLSRKFTWCYGPVAVSYLDLASVDSCEENSVLEIIA 356
 QY 360 FICKSPHRRHVRVLEPLNKLQAKMDLIPKFFLNLCLIMFTTANAYHOPTLKQA 419
 DB 357 FICKSPHRRHVRVLEPLNKLQEKMDRLIPREFNFACLYVMIIFTIYAHQPSLEQPA 416
 QY 420 APHLKAENVSMILTGHIILLLGTYLLVGOLMVFMRHVFMTWISFIDSYFELLFQAL 479
 DB 417 TSSKATREDSMLLGHILLLIGIYLLGOLMVFMRHRLFTWISMDSYFELLFVQAL 476
 QY 480 LTVASQVLCFLAIEMYLPLVASLVGLMNLVYTRGFOHTGIYSVMIQKVLRLDLLRL 539
 DB 477 LTVLSQVLRFEVEEMYLPLVASLVGLMNLVYTRGFOHTGIYSVMIQKVLRLDLLRL 536
 QY 540 LLYLVFLFEGFANALVLSQSEARPREAPTGPATETSYQPMQEGDESGNQYIGILEASLE 599
 DB 537 LLYLVFLFEGFAALVLSLSREARSPKAPENSNTVTEKPTLIGDEE--PVPYGIILDASLE 594
 QY 600 LKFTFGMGLLAFORLHNRGVNLLLLAVYLLTYILLNMLIALMSETVNSVATDSMGI 659
 DB 595 LKFTFGMGLLAFORLHNRGVNLLLLAVYLLTYILLNMLIALMSETVNSVATDSMGI 654
 QY 660 WKLOKAIISYLEMNGYWMCRKO--RAGVMLTVGTRPDGSPDERMCRVEEVNMAWSEQTL 718
 DB 655 WKLOKAIISYLEMNGYWMCRKRHRAGRLIKVGTGKDGIPDERMCRVEEVNMAWSEQTL 714
 QY 719 PVLCEPDSGAGVPRILENVVLASPRKEDEGASEENYVAVQLOSN 764
 DB 715 PVLCEPDSGAGITGYKKNPT---SKPGKNSASBEDHPLQVLOSH 756

RESULT 4
 Q9WUD2 PRELIMINARY; PRT; 761 AA.
 AC Q9WUD2;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE VANILLOID RECEPTOR-LIKE PROTEIN 1.
 GN VRL-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RX MEDLINE=99215558; PubMed=10201375;
 RA Caterina M.J., Rosen T.A., Tominaga M., Brake A.J., Julius D.;
 RT "A capsaicin-receptor homologue with a high threshold for noxious
 heat.";
 RL Nature 398:436-441(1999).
 DR EMBL; AF129113; AAD26364.1; -
 DR InterPro; IPR002110; -
 DR InterPro; IPR002111; -
 DR Pfam; PF00023; ank; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_REP_REGION; 1.
 DR SMART; SM00248; ANK; 1.
 KW Receptor.
 SQ SEQUENCE 761 AA; 86689 MW; 46A281183EEB672F CRC64;

Query Match 76.2%; Score 3051.5; DB 11; Length 761;
 Best Local Similarity 77.7%; Pred. No. 2.2e-232;
 Matches 598; Conservative 62; Mismatches 93; Indels 17; Gaps 7;

QY 1 MTSPPSPVFRLETTIDGGDEGSEADRGKLDGSGGLPMEHQFQEDRKFAQIRVNLNY 60
 DB 1 MTSASNPAPFRLETSDDGEGNAEVNKKGE----PPMSEPFQEDRNFSPOIKVNLNY 56
 QY 61 ----RKGTGA--SQDPNRPDRDLFNVAVSRGVPEDLAQLPEYLSKTSKYLTDSYTGSGT 115
 DB 57 IKRPKNTSAPSQQEDPNRPDRDLFSVYSRQVPEELTGLLEYLRNMSKYLTDSYTGSGT 116
 QY 116 GKTCLMKAVLNLDQGVNACILPLQLIDRDSGNPQPLVNAQCTDDYRQSHALIAIEKRS 175
 DB 117 GKTCLMKAVLNLDQGVNACILPLQLIDKSGNPKPLVNAQCTDEFYRQSHALIAIEKRS 176
 QY 176 LQCVKLLEVNGANVHAACGRFFQKGGTCTFEGELPLSLAACKTQMDVYVSYLLENHQAP 235
 DB 177 LQCVKLLEVNGADVHLRACGRFFQKHQGTCTFEGELPLSLAACKTQMDVYVSYLLENHQAP 236
 QY 236 ASIQATDSQGTNVLHALVMTSDNSAENIALVTSMDGLQAGARLCTPVQEDIRNLQDL 295
 DB 237 ASIQATDSQGTNVLHALVMTADNSPENSALVIMYDGLLQMGARLCTPVQEDIRNLQDL 296
 QY 296 TPPLKLAAGCKIEIFRHILOREFSG--LSHLSRKFTWCYGPVAVSYLDLASVDSCEENSV 354
 DB 297 TPPLKLAAGCKIEIFRHILOREFSGPYQPLSRKFTWCYGPVAVSYLDLASVDSCEENSV 356
 QY 355 LELIAPHCKSPHRRHVRVLEPLNKLQAKMDLIPKFFLNLCLIMFTTANAYHOPT 414
 DB 357 LELIAPHCKSPHRRHVRVLEPLNKLQEKMDRLIPREFNFACLYVMIIFTIYAHQPSLEQPA 416
 QY 415 LKQAPHLKAENVSMILTGHIILLLGTYLLVGOLMVFMRHVFMTWISFIDSYFELLF 474
 DB 417 LQGPALPSSKATPFGESMLLGHILLLIGIYLLGOLMVFMRHRLFTWISFIDSYFELLF 476
 QY 475 LFOALLTVVSOVLCFLAIEMYLPLVASLVGLMNLVYTRGFOHTGIYSVMIQKVLRL 534
 DB 477 LFOALLTVVSOVLRFEVEEMYLPLVASLVGLMNLVYTRGFOHTGIYSVMIQKVLRL 536

OY	535	LRLRELLIVLVEFEEFAVALVLSOEARPRAPPTNPNTTESQOPPEGEDGNGAKVRGIL	594
Dd	537	LRLRELVLVLFEGFAVALVLSLEANSKPKPEDNNSTVTBPPVGDEE- -BPRTSIL	594
OY	595	EASLELFKEFTIGMELAFQEOBLHRCGNVLLLLAYLVLLTYILLNMLIALMETSVSVAT	654
Dd	595	DASLELFKEFTIGMELAFQEOBLRFRGVLLLLLLAYLVLLTYVLLNMLIALMETSVNVAD	654
OY	655	DSWSIWLKOKAISYLEMBENGWMC-RKKORAGWLVLYGTCPDGSPPDERWCFFRYEBENMAS	713
Dd	655	NMSWIWLKOKAISYLEMBENGWMCRRKKHREGRLKLKGTGGDDGTPDERMCFRYEEVNMAA	714
OY	714	WEOTLPTECEDPSGAGVPRTLLENVULASPREDDEDGSEENVUYOLOVS	763
Dd	715	WEKTLPTESDPSCGPGLTKNKNT-----SKPGNSNSEEDNHLPLOYLOS	760

00	RESULT	5	
01	Q90YH8		
02	ID	Q90YH8	PRELIMINARY;
03	AC	Q90YH8	PRT; 761 AA.
04	DT	01-MAY-2000 (TREMBLrel. 13, Created)	
05	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
06	DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	
07	DE	STRETCH ACTIVATED CHANNEL 2B.	
08	GN	RSAC2B.	
09	OS	Rattus norvegicus (Rat).	
10	OC	Eukaryota; Metazoa; Chordata; Cranialata; Euteleostomi;	
11	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
12	OX	NCBI_TaxID=10116;	
13	RN	[1]	
14	RP	SEQUENCE FROM N.A.	
15	RA	Ishibashi K.;	
16	RL	"Molecular cloning of a stretch activated channel from rat kidney.";	
17	RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.	
18	DR	EMBL; AB029330; BAA88637.1; -;	
19	DR	InterPro; IPR002110; -;	
20	DR	InterPro; IPR002111; -;	
21	DR	Pfam; PF00023; ank. 3.	
22	DR	PROSITE; PSS00088; ANK_REPEAT. 1.	
23	DR	PROSITE; PSS0297; ANK_REPEAT_REGION. 1.	
24	DR	SMART; SM00248; ANK. 1.	
25	Q0	SEQUENCE 761 AA; 86705 MW; 8977CDEID5351EC8 CRC64;	

Query Match	76.0%;	Score 3041.5;	DB 11;	Length 761;
Best Local Similarity	77.5%;	Pred. No. 1.4e-231;		
Matches 597;	Conservative 62;	Mismatches 94;	Indels 17;	Gaps 77;

[illegible]

Qy	355	LEIIAIFHCSPHRRHMYVLEPLNKLLDAKMDLLIPKFLNPLCLUYMFLFTAAHYOPT	414
Db	357	LEIIAIFHCSPHRRHMYVLEPLNKLLDAKMDLLIPKFLNPLCLUYMFLFTAAHYOPT	416
Qy	415	LKQAAPELKAENVNSMLTGHLLLLGGIYLLVGOUMYEMRRHVFTWISFIDSYPEILF	474
Db	417	LDQPAIPSKATPQESMILLGHLLILGGIYLLVGOUMYEMRRRLFTWISPDMSYELF	476
Qy	475	LFQALLVYVSOYLCFLAIEMYLPLVLSALVGLMNLLYTRGFOHTGIYSVMIOKYLTD	534
Db	477	LLQALLVTSQVLEPFEMETEWLPLTVLSVGLMNLLYTRGFOHTGIYSVMIOKYLTD	536
Qy	535	LLRFLLLIYVLFPEFAVALVLSQEAARPRAPTRGNMTESQVPMQEGEDGNAQVCGIL	594
Db	537	LLRFLLLIYVLFPEFAVALVLSSEARSPKAPBEDNNSFVQEPVGOEE--PAPRSHL	594
Qy	595	EASLELEFKETIGMELEAFQEOELHRCGVLLDLLLAVYLTYILLNMLIALMSEFVNSAT	654
Db	595	DASLELEFKETIGMELEAFQEOELHRCGVLLDLLLAVYLTYILLNMLIALMSEFVNSAD	654
Qy	655	DSWSIWKLOKAI SVLEMEENGYYMWC--RRKORAGVMLTVGTRPDGSPDERMCFVAEVNMAS	713
Db	655	NSMSIWKLOKAI SVLEMEENGYYMWCRRKKNHREGRLLKGTGKGDDGPRDERMCFVAEVNMMA	714
Qy	714	MEQPLPTLCEBPGAGVPRILENVVLA SPRKEDBDGASEENYVYVUOLLS	763
Db	715	WEKTLPTLSEBPGATIGANKKNPT--SKPGNSASSEEDNHLPLVUOLLS	760

RESULT 6		PRELIMINARY:		PRT; 762 AA.	
ID	Q9JMI8				
AC	Q9JMI8				
DT	01-OCT-2000 (TrEMBLrel. 15, Created)				
DT	01-OCT-2000 (TrEMBLrel. 15, last sequence update)				
DT	01-MAR-2001 (TrEMBLrel. 16, last annotation update)				
DE	ION CHANNEL.				
OS	Rattus norvegicus (Rat).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eueleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=KIDNEY;				
RA	Suzuki M.;				
RT	"Ion channel.";				
RL	Submitted (Jan-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AB022332; BAA93435.1; -.				
DR	InterPro; IPR002110; -.				
DR	InterPro; IPR002111; -.				
DR	Pfam; PF00023; ank. 3.				
DR	PROSITE; PSS0088; ANK_REPEAT. 1.				
DR	PROSITE; PSS0297; ANK_REPEAT_REGION. 1.				
DR	SMART; SM00248; ANK. 1.				
QO	SEQUENCE 762 AA; 86767 MW; CE0970BC4195351E CRC64;				

Query Match	75.68;	Score 3028.5;	DB 11;	Length 762;
Best Local Similarity	77.48;	Pred. No. 1.5e-230;		
Matches 594;	Conservative 62;	Mismatches 94;	Indels 17;	Gaps 7;

QY 1 MTSPPSSVPFLFLETLDSGGGEGSSADNGKLTDFGSLGPPMSPOGEGDRKAPAPRVNLN 60
Db 1 MTSASSPPAFPLELSDDEDEGNMAEVNKGKQE----PPMSPQEDRBRNSPQIKAVNLNF 56
QY 61 ----RKGTGA-SQDPNPRFDRDLFNNAVSKCPVPDLAGLPBYLTSKSKYLTDSERYTGGST 115
Db 57 IKRPPKNTSASQOEPRDFEDRLFLSVYSKRPBELLGLLETRYKWNKYLITDSAYTEGST 116
QY 116 GKTCLMRAVLNLMKGVNACILPLLQIDIRDSGNPPPLVNAOCTDDTYRGRSHALHIAIEKRS 175
Db 117 GKTCIMRAVNLQGVNACIPLPQIDIKDSGNPPLVNAOCTEFYFGSHALHIAIEKRS 176

Query Match	41.3%;	Score 1652;	DB 11;	Length 838;
Best Local Similarity	46.3%;	Pred. No. 8e-122;		

Matches	359;	Conservative	127;	Mismatches	230;	Indels	60;	Gaps	15;
QY	18	GOEDGSEADRGKLDGSGLPMESEFOGEDRRKFAPOIRVN---	LNTRKGTG-----	65					
Db	51	GKGDSEES-----	-PLDCPYEGGGLASCGIITVSSVLTATQREGDGPASVPSQ	99					
QY	66	-----ASQDPRNRPDRDLNFNVSRGVPEDDLGLGPEYLSKTSKYLTDSEYTGSGTKTLM	121						
Db	100	DVSNGKEPPLIDRSTRFTDVAVSGNCELSLPLFDORSKRRLTDSFKRPEYGTCTLL	159						
QY	122	KAVLNKDGVNACILPLLDIDRDSGNPQPLVYNAOCTDDYRGHSALTAIEKRSLOQVYL	181						
Db	160	KAMLNLRHGQDITALLLDVARKTDSLKQFVNASYSDSYVKGQFALHAIERNNVTLT	219						
QY	182	LVENGANVAHARACGRFFQKGG-TCFYTGELPLSLAACKTQMDVSYLLENPHQASIQ	240						
Db	220	LVENGADVQAANGDFEKKTRGPRGVEYGEPLPLSLAACKTNLAIVKFLFLONSWOPADISA	279						
QY	241	TDQSGNTVHLVMSDSASENIALVTSMYGLOLAGARLCTVQLEDIRNLQDITPLKL	300						
Db	280	RDSQGNVTLVHLVADYADNTVDTKFVMTMYNEILTLGKLAHPTLLEETNRKGLTPAL	339						
QY	301	AAKEKIEIFRHILQREF--SGLSHLSKRTTWCYGPVRSVLDIASVDSCEENSLEIT	358						
Db	340	AASSKIGVLAIVTIORELHEPECRHLSSKPTFEMAAGVPHSSLYDSCIDTECKNSVLEVI	399						
QY	359	AF-HCKSPRRHRMVLLEPLNKLLOAKWDLIPK-FELNPLCNLIYMFPTAVAVHQPTLK	416						
Db	400	AYSSETFENRHMLVEPLNRLLODKMRFVYKRIYFNFVEYCLYMIIFTAAAYRPV--	457						
QY	417	KQAAP--HLKAEVGSMLTGHILLGLGIYLVQOLWTFMRNHFVMTSFDSEFELF	474						
Db	458	EGLPYRLKNTVGGYFRTGTGELISVSGVYFFRGIOYFLQRRPSLSLFPVDSLELIF	516						
QY	475	LEQALLTVASOVLCELAIEWYLPLLVSALVLCWMLNLTLYTRGFQHTGYSVMIQKVIIRD	534						
Db	517	FVQSGFMLVSVLYRSQKEKYAVSNVPSLAKMTMMLYTRGFQMGITAVAMIEKMLIRD	576						
QY	535	LIRFLILVLELGFVAVALVLSLQEMRPEADPTGNATESVQPMEGQDEGNCA-----	588						
Db	577	LCRFMFVYLVLEFGSTAVLTLED-----GKN---NSLPMESTPHKCSACKPGN	625						
QY	589	OYRGLESLSELFKTTIGMGLARPODLHFRGNVLLLLAYVLLVYIILNLTLMSET	648						
Db	626	SYNSLSTYCLCEFKFTTIGMGLFEFENYDEKAVFTILLAVYILYITLNLNLTLMSET	685						
QY	649	VNSVATDSMSIKRLQKATLSVLEMNGYMW-C-RKKORAGVMLVYGTIKDSDPERACFRYE	707						
Db	686	VNKIOESKNIKRLOKRAITITLDTKSFCLKMKARRSKGLLOVGTTPDCKDXYRNCFRD	745						
QY	708	EYVNAWSWQETLPTCEDPSGA-GVPTRELPVPLASPKEDDGASEENYVPVOLLQ	762						
Db	746	EVNMTTMTNVGIIINEDPNCNCGVARTLSFSLRG----RVSGRMWKNFALVPLLR	797						
RESULT	8								
Q9JMS7	PRELIMINARY:	PRF:	838	AA.					
AC	Q9JMS7:								
DT	01-OCT-2000 (TREMBlrel. 15	Created)							
DT	01-OCT-2000 (TREMBlrel. 15	Last sequence update)							
DT	01-MAR-2001 (TREMBlrel. 16,	Last annotation update)							
DE	VANILLOID RECEPTOR TYPE 1	LIKE PROTEIN 1.							
GN	VRIL1.								
OS	Rattus norvegicus (Rat).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.								
OX	NCBI_TaxID=10116;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RA	Tsutsumi S., Nakamura A., Kohama K.;								
RT	"Vanilloid receptor type 1 like protein 1."								
RL	Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.								


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OY 548 GFAVALVSLSOEA-----WRPEAPTPGNATESVQPMEOGEDGNGAQRGIL 594
DB 590 GFTAVAVTLIEDCKNDLSLSESTSHMRGACRPDSS-----YNSLX 632
OY 595 EASLELFKFTIGGELAFQDQLHFRGMVLLLLAYVLLYLLLNLMALMSTVSVAT 654
DB 633 STCLELFKFTIGGDELFEFENYDFKAVFIILLAYVLYILLNLMALMGETVAKIAQ 692
OY 655 DMSIKRLKAIISVLEMENGYMWC-RRKORAGVMTVGTGPDGSPDERCFRVEEYNNM 713
DB 693 ESKNIMKLOKRAITLIDTEKSFELCKMKRFRSGKLVGYTPDGKDDYRMCFRVDEVNMTT 752
OY 714 WEOTLPTLCEDPSCA-GVPTLTLENPVLASPPKEDGASEENYVPVQLQ 762
DB 753 WNNVGIINDEDPNCGEVKRTLSFSLRSS----RVSGRHKMKNALVPLLR 798

RESULT 12
O9NF22 PRELIMINARY; PRT; 839 AA.
AC 09NF22;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE VANILLOID RECEPTOR 1.
GN VRL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=PORESAL ROOT GANGLION;
RA McIntyre P., Winter J., Phillips E., Webb M., Chambers A.,
RA Meeseckera N., Rang H., Savidge J., Clarke M., James I., Bervan S.,
RA McLatchie L., Rang H., Savidge J., Clarke M., James I., Bervan S.,
RA "Pharmacological comparison of human and rat VRL expressed in CHO
RT cells."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ272063; CAB89866.1; -.
DR InterPro: IPR002110; -.
DR InterPro: IPR002111; -.
DR Pfam: PF00023; ank; 3.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR SMART: SM00248; ANK; 1.
KW Receptor.
SQ SEQUENCE 839 AA; 94939 MW; CCOD93A3AAD725F8 CRC64;

Query Match 40.9%; Score 1636.5; DB 4; Length 839;
Best Local Similarity 48.2%; Pred. No. 1.3e-120;
Matches 342; Conservative 122; Mismatches 201; Indels 45; Gaps 11;

OY 74 FDRDLRFNAVSRGVPDLGLPEYLSKTSKYLTDSSEYTGSTGTCMLKAVLNKDGVA 133
DB 113 YDRSIFFEAVAOONNCDLSLFLFLOKSKKHLTDNEFKDPETCTCLKMLNHDGONT 172
OY 134 CILPILQIDRDSGNPPQVNAOCTDDIYGRGSHLHAIERKSLQCYKLVLENANVHARA 193
DB 173 TLPLELEIKRQDLSKELVNAASYDYSYKQDTLHAIERNNALVTLLENADADQAAA 232
OY 194 CGRFQKGGG-TCGYFGEGLPLSLACTKQMDVSYLLENHOPASLOATDSDGNTLHAL 252
DB 233 HGDFEKKTKGRPFYTGELPLSLAAGTNGIGYKFLIÖNSWÖTADISARDSGNTVLHAL 292
OY 253 VMSDMSAENIALVTSWYDGLQAGARLCPVQLEDIRNLQDITPLKLAKKEGKIFFRH 312
DB 293 VEADATADTKRVTSMYNEIILGAKLHPTLKEELTNKKGMPLALAAAGTKICVLAV 352
OY 313 ILQRETS--GLSLSKKFTKCYGPRVSLYDLASVSCENSVLEIIAF-HCKSPHRRH 369
DB 352 ILQRETS--GLSLSKKFTKCYGPRVSLYDLASVSCENSVLEIIAF-HCKSPHRRH 369

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DB 353 ILQREIOPEBCRLSKRFTEMAYPVHSSLYDLSCIDTECKNSVLEVIAYSSSEPRNRD 412
OY 370 MVLVEPLNLKLOAKWDLIPK-PELNFELCNLYMFIETFAVAYQPTLKKQAAPHLKAE-V 427
DB 413 MLVEPLNLKLOAKWDLIPK-PELNFELCNLYMFIETFAVAYQPTLKKQAAPHLKAE-V 469
OY 428 GNSMLTGLHLLGCIYLLVGLWYFMRHVFIMWISDFEELFLQALTTVSOVL 487
DB 470 GDYFVATGELISLVGVEFFERIGIYFLQKRPMSKTLFVDSYSEMLFQISLEFMTAVYL 529
OY 488 CFLATEWYLPILVASVAVLGNLNYTTRGFQHTGTSVMIQKYLIDRLFLIYVLELF 547
DB 530 YFSHLEKYVASWVSLALMTNMLYTTTRGFQHTGTSVMIQKYLIDRLFLIYVLELF 589
OY 548 GFAVALVSLSOEA-----WRPEAPTPGNATESVQPMEOGEDGNGAQRGIL 594
DB 590 GFTAVAVTLIEDCKNDLSLSESTSHMRGACRPDSS-----YNSLX 632
OY 595 EASLELFKFTIGGELAFQDQLHFRGMVLLLLAYVLLYLLLNLMALMSTVSVAT 654
DB 633 STCLELFKFTIGGDELFEFENYDFKAVFIILLAYVLYILLNLMALMGETVAKIAQ 692
OY 655 DMSIKRLKAIISVLEMENGYMWC-RRKORAGVMTVGTGPDGSPDERCFRVEEYNNM 713
DB 693 ESKNIMKLOKRAITLIDTEKSFELCKMKRFRSGKLVGYTPDGKDDYRMCFRVDEVNMTT 752
OY 714 WEOTLPTLCEDPSCA-GVPTLTLENPVLASPPKEDGASEENYVPVQLQ 762
DB 753 WNNVGIINDEDPNCGEVKRTLSFSLRSS----RVSGRHKMKNALVPLLR 798

RESULT 13
O9DFE3 PRELIMINARY; PRT; 852 AA.
AC 09DFE3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE VANILLOID RECEPTOR-RELATED OSMOTICALLY ACTIVATED CHANNEL PROTEIN.
GN VR-OAC.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=COCHLEA;
RX PubMed=11081638;
RA Liedtke W., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S., Sali A.,
RA Hudspeeth A.J., Friedman J.M., Heller S.,
RA "Vanilloid Receptor-Related Osmotically Activated Channel (VR-OAC), a
RT Candidate Vertebrate Osmoreceptor."
RL Cell 103:525-535(2000).
DR EMBL: AF261883; AAG28026.1; -.
KW Receptor.
SQ SEQUENCE 852 AA; 96197 MW; E8365D3FAD08C1 CRC64;

Query Match 36.6%; Score 1467; DB 13; Length 852;
Best Local Similarity 41.7%; Pred. No. 3.3e-107;
Matches 338; Conservative 121; Mismatches 245; Indels 106; Gaps 14;

OY 23 SEADRGLKLPDGSGLPMESQFQEDKRPQIRVNVN----- 58
DB 37 AEPSSKGPAGAGDKONLRMKFHGAFRRKGPMPLELSTYESSVVPAPKAPMDSLFDY 96
OY 59 -MYRK-----GTGASQDP-----NRRDRRLFNVAASRGVPEDLAIP 95
DB 97 GTYRQHPSENKMKRRRVRVEKPAVAGTGAPAPNPVPLVKNRPTLFDIVSRGSDGLEGLL 156
OY 96 EYLSKTSKYLTDSSEYTGSTGTCMLKAVLNKDGVAICILPQIDRDSGNPQPLVNAO 155
DB 155 EYLSKTSKYLTDSSEYTGSTGTCMLKAVLNKDGVAICILPQIDRDSGNPQPLVNAO 155

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Db 157 SELLTHKKRLTDEEFREPSTGKTCPLKALLNLSAGHNDTIPILLDIAEKTGNMREFINSP 216
Qy 156 CTDDYRGRSALHIAIERKSLQCVKLLVNGANVHARACGRFQ--KGQGTCTFFGGLPLS 214
Db 217 FRVYVYRGOTAHIAIERCKKHVELLVERGADVQAAGRFQOPDEGFFGGLPLS 276
Qy 215 LAACQOMQVSVSYLLENPHQASLOATDSOGNTVLHALVMSIPNSAENIALYTSMTDGL 274
Db 277 LAACQOMPHIVHLENTGNGKQADLRQDSRGNTVLHALVAIDNTENKRFYTKMDDL 336
Qy 275 QAGARLCPTVOLEDIRNLODLPPLKAAEGKIEIFRHILQREFS--GLSHLSRKFTMC 332
Db 337 IKCAKLEFPTNLEALNNDCGLSPMAAATGKIGIFQHIIRREIAEDVRRHLSRKDMA 396
Qy 333 YGPRVRSLYDLASVSC--EENSYLETIAFRCKSPHRRHNVLEPLKLLQAKDDL--IKR 390
Db 397 YGPRVRSLYDLASVSC--EENSYLETIAFRCKSPHRRHNVLEPLKLLQAKDDL--IKR 390
Qy 391 PFLNFCNLTYMFIPTAVVYHOPTLKKQAAPHLKAEVNSMLTGHILLGLGTYLLVGQ 450
Db 457 FTVSVSYLCAMITFLAYRR--MEGPPRYTTTIDYLRAGLITILLGILFFESN 514
Qy 451 LW-YEMRRHVFIIWISFIDSYFELLFLFOALLTVVSGVLCFLAIEWYLPPLVSALVGMWN 509
Db 515 IKDLFMRKCPGVNSPFIIDGSPFQLYFYSVLVYTAGLYGVEAYLVAVFALVGMWN 574
Qy 510 LLYTTFPGHGTGYSMIOKVILRDLRLLYLVLFEGFAVALVL-----SOE 559
Db 575 ALYFRGGLTGYTSIMIKILFKDLFRLLYLVLFMIYASALVSLMPCPSSSCSD 634
Qy 560 AMRPAEPTGNATESVQPMEOGDEGNGAQYRGILEASLELEFRTGMGLAFOFOLHR 619
Db 635 HSNCTIPTPSCRDS-----QTFSTFLDLDFKLTIGMDLMELESAKIP 678
Qy 620 GAVLLLLAYVLLTYLLNMLALMSETVNSVADSWMSIMLOKASVLEMEGY--MMC 678
Db 679 GVEIILLVLYIILFEVLLNMLALMGEITGVGVSKESKHIMLOMATYLLDIERSPFL 738
Qy 679 RKORAGVMLTYGTRKDGSPDERMCFRVEEVMNASWEOQLPTLCEPDSAG----- 729
Db 739 RRAFSGEMVYQKGTIDGPPDRMCFRVEEVMNASWNOMLGITSEDPKSDTYQYGFESH 798
Qy 730 -----VPRTEENPYLASPPKED 746
Db 799 TVGRLRRDRMSTVPRVVE--LNKSCPTED 826

RESULT 14
Q9HBC0 PRELIMINARY; PRT; 871 AA.
AC Q9HBC0:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
DE 01-MAR-2001 (TREMblrel. 16, last annotation update)
DE OTRPC4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE=RENAL CORTEX;
RX PubMed=11025659;
RA Stromann R., Harteneck C., Nunnenmacher K., Schultz G., Plant T.D.:
RT "OTRPC4, a nonselective cation channel that confers sensitivity to
DR extracellular osmolarity."
RL Nat. Cell Biol. 2:695-702(2000).
EMBL: AF258465; AAG16127.1;
SEQUENCE 871 AA: 98294 MW; C62056B8D6A6FB6 CRC64;

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Query Match 36.6%; Score 1467; DB 4; Length 871;
Best Local Similarity 43.1%; Pred. No. 3.4e-107;

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Matches 339; Conservative 114; Mismatches 246; Indels 88; Gaps 16;
Qy 8 PVFRLETLGGQEDG-----SEADRKG-LDFGSLPMPESQFQGEDKRP----- 52
Db 32 PLSLNLNLEG--EDGLSPSPADASRPAGPGRPLRMKFOGAFKGPVNPIDLESTL 90
Qy 53 -----QIRVNLNRYK-----GTGASOPDP--NRPD 75
Db 91 YESSVYPCRRKAPMDSLFDTGYTRHHSNDKRRKKIIEKQPOSAPAPAPDPPILKVEN 150
Qy 76 RDLFNVAASRGVPEDLAGEPEYLSKTSKYLTDSYEGSTGKTCMLKAVNLKDGVNACI 135
Db 151 RPLFDIVASRGSTADLDGLLPFLTHKKRLTDEEFREPSTGKTCPLKALLNLSNGNDTI 210
Qy 136 LPLLOIDRDSGNPQPLVNAQCTDDYVYRGSAHIAIERKSLQCVKLLVNGANVHARAC 195
Db 211 PVLDDIAERTGNMREFINSPFRDIYRGOTAHIAIERCKKHVELLVERGADVQAAG 270
Qy 196 RFPQ--KGQGTCTFFGGLPLSIAACTQOMQVSVSYLLENPHQASLOATDSOGNTVLHALV 254
Db 271 RFPQKDEGCTFFGGLPLSLAAGTQPHIVNLTENPHKKADMRQDSRGNTVLHALVA 330
Qy 255 ISDNSAENIALYTSMTDGLQAGARLCPTVOLEDIRNLODLPPLKAAEGKIEIFRHIL 314
Db 331 IADNTENKRFYTKMDDLKCARLFPDSNLVAVLNNDGLSPMAAATGKIGIFQHI 390
Qy 315 QREFS--GLSHLSRKFTMCYGPVRSLYDLASVSC--EENSYLETIAFRCKSPHRRHV 371
Db 391 RREVYDEDRHLSRKFKDMAVGPVRSLYDLASVSLDSCGEASVLELYVNSKIENHEML 450
Qy 372 VLEPLKLLQAKDDL--IKRFLNFCNLTYMFIPTAVVYHOPTLKKQAAPHLKAEVNS 430
Db 451 AVEPIINELLRDKRRKGAVSFIINVSYLCAMITFLAYRPL--EGTPPYRTTYVY 508
Qy 431 MLTGHILLGLGTYLLVGMQL--YEMRRHVFIIWISFIDSYFELLFLFOALLTVVSGVLC 489
Db 509 LRLAGVITLTFGVLPFFPINIKDLFMKCPGVNSPFIIDGSPFQLYFYSVLVYSAVL 568
Qy 490 LALIEWYLPPLVSALVGMWNLYYTRGPHGTGYSMIOKVILRDLRLLYLVLFEGFA 549
Db 569 AGIEAVLAVVAVLVGMWNALYFTRGKLTGYTSIMIKILFKDLFRLLYLVLFMIY 628
Qy 550 AVALVSL-----SOEAMRPAEPTGNATESVQPMEOGDEGNGAQYRGILEASLE 599
Db 629 ASALVSLNLPKANMKVCNEDQNTCTPYTPSCRDS-----ETFSFLL--LD 672
Qy 600 LRFETIGMGLAFQEOHLHFRGVLLLLAYVLLTYLLNMLALMSETVNSVADSWMSI 659
Db 673 LFKLTIGMDLMLSTSKYPVVFIIILTYIILFEVLLNMLALMGEITGVGVSKESKH 732
Qy 660 KRLQKASVLEMEGY--MMCRRKORAGVMLTYGTRKDGSPDERMCFRVEEVMNASWEO 718
Db 733 KRLQWATYLLDIERSPFLRAFRSGEMVYQKGTIDGPPDRMCFRVEEVMNASWNOML 792
Qy 719 PTLCEDP 725
Db 793 GIINEDP 799

RESULT 15
Q9ERZ8 PRELIMINARY; PRT; 871 AA.
AC Q9ERZ8:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
DE 01-MAR-2001 (TREMblrel. 16, last annotation update)
DE VANILLOID RECEPTOR-RELATED OSMOTICALLY ACTIVATED CHANNEL.
GN VROAC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 111

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RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX Pubmed=11081638;
RA Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RT Sali A., Hudspeth A.J., Friedman J.M., Heller S.;
RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RT candidate vertebrate osmoreceptor.";
RT Cell 103:525-535(2000).
DR EMBL; AF263521; AAG28027.1; -.
KW Receptor.
SO SEQUENCE 871 AA: 98009 MW: 5D50684DA08C354B CRC64;

Query Match 36.6%; Score 1465.5; DB 11; Length 871;
Best Local Similarity 40.4%; Pred. No. 4.5e-107;
Matches 341; Conservative 128; Mismatches 257; Indels 119; Gaps 16;

QY 8 PVPRLETLGGGQEDGS-----EADRGKLPFGSLPMESEFOGEDRRKAP-----52
DB 32 PLSSLANLFEGERGSSSLSPVDASR--PAGPGDGRPNLRMKFGCAFRRKGVNPIIDLESTL 90
QY 53 -----QIRVNLNVRKGTGASQDPNRR-----FD 75
DB 91 YESSVYVPGRRKAPMDSLFDYGYTRHHPSDKKRRKRVVEKOPSPKAPAPOPPIIKVFN 150
QY 76 RDRLENAVSRGVPEDLAQLPEYLKSTSKYLTDSYEGSTGKTCLMKAVLNKGVNACI 135
DB 151 RPILFDIYVRGSGTADLDGLSTYLTTHKKRLTDEFEFREPSTGCTCLPKALLNLSNGRNDTI 210
QY 136 LPLQLIDRDSGNPQPLVNAOCTDDYRGHSALHIAIEKRSLOQCVKLLVENGANVBARACG 195
DB 211 PVLLDIAERTGNMREINSPFRDIYRGQTLHIAIERCKHYVELLVAQADVHAQARG 270
QY 196 RFFQ-KGOGTCFEGELPTSLACTKQWVSYLLENPHOPASLOATDSOGNTVLHAIYM 254
DB 271 RFPQKDEGTYRFGELPLSLACTQPHIVNLTENPKKADMRDSDRGNTVLHALVA 330
QY 255 ISDNSAENIALVTSMYDGLLAGARLCPVOLEDIRNLQDLTPKLAAEGKTEIFRHIL 314
DB 331 IADNTRENTKFTVKMYDILLKCSRLFPDSNLETVLNNDGLSPLMAAKTGKIGVQHII 390
QY 315 QREFS--GSHLSRKTEWCYGPVRSYLDLASVDSG--EENSYLELIAFHCKSPRRHRV 371
DB 391 RRRVVDDETRHLSRRKKDMAYGVSYSLLDLSLDTCGEVSYLEIVNYSKIRNHEML 450
QY 372 VLEPLNKLQAKMDLL-IRKFLNFCNLTYEIFTAVVAHOPTLKKQAAPHLKAEVGS 430
DB 451 AVEPIINELLRDKRRKRGAVSFYINVSYLCAVYITLTAYQPL--EGTPPYRTTYDY 508
QY 431 MLTGHILLILGGIYLVGOLW-YEMRRHVFIMWISFIDSYFEILLFLOALLTVVSOVLCP 489
DB 509 LRLAGEVITLLGVLFEFFSIRKDLPMKKCPGVNSLFVDSGFOLLYFSVLVVSAAVL 568
QY 490 LAIEWLPLLVSAVLVGMNLXYTRGFQHTGYSVMIOKAVILRDLRLFLLYVFLBGF 549
DB 569 AGIEAVLAVVAFALVGMNALYFTRGTLGTYSIMIQILFKDLFRLLVLYLLEFMIGY 628
QY 550 AVALVSL-----SOEAWRPEAPRTGPNATESVQPMEGQDEGNGAQYRGITLASLE 599
DB 629 ASALVTLILNPTNMKVCNEDQNCYPSIPACRDS-----ETFSAPL--LD 672
QY 600 LRFKTIQMGELAFQOLHRCGVLLLLLVVLLTYILLNMLIALMSETVNSVATDSWSI 659
DB 673 LFKLTIGMDLEMLSSAKYPVVEIILLVYIILTFVLLNMLIALMGETVGQVSKESKHI 732
QY 660 WKLOKAISYLEMENGY-WMCRKKORAGVMLYVTKPDGSPDERMCFRVEVNMASWEOQL 718
DB 733 WKLOWATITLIDERSFPVFLRKAFRSGEVMTVGKSSDGTDDRWCFRYDEVNMSHNQNL 792
QY 719 PTLCEDDPS-----GAGVPTLENPVLASPRKDEDDGASEENY 756
DB 793 GIINEDPGKSEIYQYYGSHMGRLRRDRWSSVPRVVE-----LNKNSGTEVVV 843

QY 757 PVQLL 761
DB 844 PLDNL 848

Search completed: July 18, 2001, 16:00:08
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